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Research Article

Morphological and phylogenetic characterization of three new *Cortinarius* (Cortinariaceae, Agaricales) species in Yunnan, China

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Abstract

Through comprehensive morphological and phylogenetic investigations (ITS and nrLSU), we have delineated three novel species within *Cortinarius*, as derived from specimens collected in Yunnan Province, China. *Cortinarius mucobrunneus* is distinguished by its viscid basidiomata, dark brown pileus adorned with translucent stripes, cinnamon to brown lamellae, white stipe leaving a cinnamon ring on the upper part, and elliptical to amygdaliform, strongly verrucose basidiospores measuring 13.5–16 × 8–10 µm. *Cortinarius rugosiviscidus* is characterized by sticky basidiomata, a light brown pileus with wrinkled surface, brown lamellae, light brown stipe, and elliptical to amygdaliform, moderately verrucose basidiospores measuring 11.5–15 × 7.5–9.5 µm. *Cortinarius saloroides* is characterized by its violet pileus with fine fibrous scales, mauve to light brown lamellae, bluish violet stipe leaving a light brown ring on the upper part, and subspherical, broadly elliptical to elliptical, moderately verrucose basidiospores measuring 7–8.5 × 5.5–6.5 µm. Differences between the new species and morphologically similar and phylogenetically related species are discussed.

Key words: Morphology, new taxa, sect. *Delibuti*, sect. *Defibulati*

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Introduction

Cortinarius (Pers.) Gray is one of the most species-rich genera in the phylum Basidiomycota R.T. Moore. More than 5,881 records of *Cortinarius* are listed in Index Fungorum (https://www.indexfungorum.org/Names/Names.asp, accessed on 25 August 2025). Its taxonomic history can be traced back to Persoon (1801), who first described it as a section within the genus *Agaricus* L., and later Gray (1821) elevated it to the rank of an independent genus. This genus exhibits distinct morphological characteristics, which comprise a gleaming luster on the surface of the fruiting body, a cobweb-like veil present between the pileus and stipe during its juvenile stage, and mature basidiospores that range from rusty brown to brown, characterized by a warty surface texture (Moser and Horak 1975; Singer 1986). While macroscopic morphology is generally easily identifiable, the subtle morphological differences among species have posed significant challenges for traditional classification. In recent years, the

meticulous investigation of morphology, coupled with molecular phylogenetics, has emerged as a pivotal approach for reevaluating the taxonomic framework of this genus (Seidl 2000; Soop et al. 2019; Xie et al. 2021a, 2025; Long et al. 2024).

Cortinarius exhibits a broad ecological adaptability and forms ectomycorrhizal symbiotic relationships with a wide range of woody and herbaceous plants, including Betulaceae Gray, Cyperaceae Juss., Fagaceae Dumort., Nothofagaceae Kuprian., Orchidaceae Juss., Pinaceae Spreng. ex F.Rudolphi, and Salicaceae Mirb. (Harrington and Mitchell 2002; Jacquemyn et al. 2010; Tedersoo et al. 2011; Harrower et al. 2015; Thoen et al. 2019). It plays a key role in forest ecosystems, regulating nutrient cycling and community stability. Some species, such as *Cortinarius armillatus* (Fr.) Fr., *C. bovinus* Fr., and *C. emodensis* Berk. possess both edible and medicinal value. However, a few species, including *C. gentilis* (Fr.) Fr., *C. orellanus* Fr., and *C. rubellus* Cooke, contain the toxin orellanine, which can cause renal failure-type poisoning upon accidental ingestion (Bau et al. 2024).

In the classification system of *Cortinarius*, sect. *Delibuti* (Fr.) Henn. and sect. *Defibulati* M.M. Moser are two important groups. Early classifications were based on the mucus characteristics of the pileus and stipe, placing them within *Cortinarius* subg. *Myxacium* (Fr.) Trog (Trog 1844; Earle 1902; Singer 1986; Seidl 2000; Garnica et al. 2005). However, molecular systematic studies by Soop et al. (2019) showed that sect. *Delibuti* is more appropriately placed within the *Anomaloid* sections. Some European scholars regard sect. *Defibulati* as a subsect of sect. *Colliniti* (Brandrud et al. 1990, 1992; Bendiksen et al. 1993). Seidl (2000) pointed out through phylogenetic analysis that sect. *Defibulati* and sect. *Myxacium* are closely related and monophyletic, while sect. *Delibuti* is on a more distant branch in the phylogenetic tree.

During a survey of fungal diversity in the Qinghai-Xizang Plateau and its surrounding areas in China, six *Cortinarius* specimens characterized by a viscid pileus were collected (Wang et al. 2025). A comprehensive morphological assessment, supplemented by detailed illustrations and descriptions, was conducted in conjunction with multi-locus phylogenetic analyses to elucidate the taxonomic status of these novel populations. Sequence data derived from the ITS and nrLSU regions revealed that these strains consistently clustered into distinct clades with robust statistical support. Morphological evaluations indicated unique distinguishing features among our specimens. Consequently, we propose three new taxa, accompanied by their full descriptions, illustrative representations, and detailed phylogenetic relationships.

Materials and methods

Sample collection

Six specimens of *Cortinarius* were collected from *Abies* forests in Yunnan Province, China, between August 2017 and August 2024. During the collection process, habitat photos were taken by digital cameras (Canon, Japan), and relevant information such as the collection location, time, altitude, longitude, and latitude was recorded (Rathnayaka et al. 2024). The specimens were described in detail in terms of macroscopic morphology, including the pileus, context, lamellae, and stipe. Some fresh specimens were dried using silica gel desiccant

for DNA extraction, while the remaining specimens were dried in a food dryer at 40 °C (Hu et al. 2022). The newly collected specimens were deposited in the Herbarium of Cryptogams of Kunming Institute of Botany, Chinese Academy of Sciences (KUN-HKAS), China.

Morphological observation

Samples were observed and examined using the method described by Zhao et al. (2015). Macroscopic and microscopic features were examined using a stereomicroscope (SteREO Discovery.V12, Carl Zeiss Microscopy GmBH, Germany), and microphotographs were taken using a compound microscope (Nikon ECLIPSE 80i, Nikon, Japan) fitted with a NikonDS-Ri2 digital camera (Nikon, Japan). Color codes indicated in the descriptions were based on Kornerup and Wanscher (1981). Dried specimens were sectioned and mounted in a 5% KOH solution and Melzer's reagent, using 5% Lugol reagent for observing iodine reaction. Congo red reagent was used for staining to facilitate observation of the microscopic structure. In order to observe the ornamentation on the surface of basidiospores, some hymenophoral fragments were cut from the dry specimens, fixed on aluminum stubs, coated with gold-palladium, and then observed under a ZEISS Sigma 300 scanning electron microscope (SEM) at the Kunming Institute of Botany.

Microstructure measurements were performed using Image Frame Work v.0.9.7. Measurements were given as (a–) b–c (–d), where a denoted the minimum value, d was the maximum value, and b–c was the 90% confidence interval. The measured number of basidiospores (n), basidiomata (m), and specimens (p) was denoted as [n/m/p]. The Q value indicated the length to width ratio of the basidiospores, while **Q** indicated the average of the length to width ratios (Q) of all ascospores ± standard deviation. The illustrations were done using Adobe Photoshop 2020 (Adobe Systems, USA).

DNA extraction, PCR amplification, and sequencing

DNA was extracted from fruiting bodies of *Cortinarius* directly using Trelief™ Fungal Genomic DNA Extraction Kit (Tsingke Biotechnology Co., Ltd., Beijing, China). Polymerase chain reaction (PCR) was used to amplify the nuclear ribosomal internal transcribed spacer (ITS) and the large subunit of the nuclear ribosomal RNA (nrLSU). Universal primer pairs ITS5/ITS4 (White et al. 1990) and LR0R/LR5 (Vilgalys and Hester 1990) were used to amplify the ITS and nrLSU loci, respectively. The PCR conditions are as follows: an initial denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 53 °C for 20 s, and extension at 72 °C for 30 s, followed by a final extension at 72 °C for 10 min. PCR products were sent to Tsingke Company in Beijing, China, for sequencing.

Phylogenetic analyses

The newly generated sequences were checked for ambiguous bases and assembled using DNASTAR Lasergene SeqMan Pro v.7.1.0. This study used new sequencing data and reliable data from the literature to construct a phylogenetic tree (Table 1), mainly referring to the research results of Soop et al. (2021),

Xie et al. (2021a), Long et al. (2024), and Xie et al. (2025). Multiple sequence alignments were aligned in MAFFT v.7 (https://mafft.cbrc.jp/alignment/server/index.html, Katoh and Standley 2013; Katoh et al. 2019), and trimmed using TrimAl v.1.3 (Capella-Gutiérrez et al. 2009). The 'gapthreshold' was set to 0.5 for both ITS and nrLSU regions. The trimmed sequences were sequentially assembled into a combined dataset using SequenceMatrix V.1.8 software (Vaidya et al. 2011).

Maximum likelihood (ML) analysis was performed in the CIPRES Science Gateway (http://www.phylo.org/) platform using RAxML-HPC2 v.8.2.12 (Miller et al. 2010). The substitution model for ML analysis of all gene regions was GTR+I+G, with 1,000 rapid bootstrap replicates. Bayesian inference (BI) analysis was performed using MrBayes v.3.2, using Markov Chain Monte Carlo Sampling (MCMC) to calculate a posterior probability (PP). MrModeltest v.2.3 (Nylander et al. 2004) was used to determine the best-fit model for the evolution of each gene using the Akaike information criterion, and GTR+I+G substitutions were ultimately selected as the appropriate models for ITS and nrLSU. Four simultaneous Markov chains operated simultaneously for 1195000 generations, and samples were taken every 100th generation. The first 25% of trees were discarded due to aging, and convergence was determined when the standard deviation of the split frequencies reached 0.01 and the effective sample size (ESS) > 200. The phylogenetic tree was visualized using FigTree v.1.4.4 and reorganized in Adobe Illustrator CC 2018 (Adobe Systems, USA).

Table 1. Names, voucher numbers, countries, references, and corresponding GenBank accession numbers of the taxa used in this study. Names in red background indicate newly described species in this study. All type specimens are highlighted with a "T". The symbol "–" denotes no available data.

Species	Voucher	Locality	GenBank Accession No.		References
			ITS	nrLSU	
Cortinarius acutovelatus	F16388	Canada	FJ039609	–	Harrower et al. (2011)
C. albocyaneus **T**	S:CFP1177	Sweden	KX302206	–	Dima et al. (2016)
C. alboluteus **T**	DAOM R. Lebeuf HRL2038	USA	NR_157977	–	Genbank
C. alpinus	HMJAU44407	China, Neimenggu	MW911727	–	Xie et al. (2021a)
C. anomalus	NL-5414	Hungary	MZ663777	–	Dima et al. (2021)
C. anomalus **T**	S:CFP1154	Sweden	KX302224	–	Dima et al. (2016)
C. basipurpureus	PERTH 04259629	Australia	AY669607	AY669607	Garnica et al. (2005)
C. bolaris	TUB 0118524	Germany	AY669596	AY669596	Garnica et al. (2005)
C. brunneoalbus **T**	TN09-075	USA	NR_153040	–	Ariyawansa et al. (2015)
C. calaisopus **T**	PDD:94050	New Zealand	NR_157880	NG_068868	Genbank
C. camphoratus	DAVFP26155	Canada	EU821659	EU821659	Harrower et al. (2011)
C. camphoratus	SMI193	Canada	FJ039626	FJ039626	Harrower et al. (2011)
C. carneoroseus	EN76 (CORD)	Argentina	JX983157	–	GenBank
C. cf. *tibeticisalor*	HMJAU58970	China, Xizang	PQ278654	PQ489285	Xie et al. (2025)
C. collinitus	IB19940257	Sweden	AY033096	AY033138	Peintner et al. (2002)
C. corpulentus **T**	DBB49315	USA	OP874939	–	GenBank
C. costaricensis **T**	JFA 11904	Germany	EF420147	–	Ammirati et al. (2007)
C. camphoratus	DAVFP26155	Canada	EU821659	EU821659	Harrower et al. (2011)

Species	Voucher	Locality	GenBank Accession No.		References
			ITS	nrLSU	
C. cuphocyboides	CO1018	Germany	AY669625	AY669625	Garnica et al. (2005)
C. cypripedi **T**	PDD107723	New Zealand	KT875199	–	Soop (2016)
C. cystidiocatenatus	HO A20518A6	Germany	AY669651	AY669651	Garnica et al. (2005)
C. delibutus	F17048	Canada	FJ717515	FJ717515	Harrower et al. (2011)
C. delibutus	SAT01-301-12	USA	FJ717513	FJ717513	Harrower et al. (2011)
C. dryadicola	HMJAU58991	China, Yunnan	PQ278684	PQ489266	Xie et al. (2025)
C. dryosalor	AB05-10-302	France	OM964840	–	GenBank
C. dryosalor **T**	FA4700	Spain	OM964838	ON032996	GenBank
C. durifoliorum **T**	PDD:101829	New Zealand	KJ635210	MW263597	Soop et al. (2018)
C. eunomalus	PDD 107706	New Zealand	KT875201	MW263617	GenBank
C. fibrillososalor	MHHNU 32070	China, Hunan	OR660685	OR647503	Long et al. (2024)
C. fibrillososalor **T**	MHHNU 32494	China, Hunan	OR647481	OR647506	Long et al. (2024)
C. gymnocephalus **T**	CO1334	Germany	AY669629	AY669629	Garnica et al. (2005)
C. illibatus	HMJAU48760	China, Heilongjiang	MW911735	OP620668	Xie et al. (2021a)
C. illibatus	OS574	Norway	KC842441	KC842511	Stensrud et al. (2014)
C. illitus **T**	IB1963414	Argentina	AF389128	AF388751	Peintner et al. (2004)
C. illumines **T**	S:F44877	Sweden	KP866156	–	Niskanen et al. (2015)
C. iodes	MQ19-CMMF003109	Canada	MN751331	–	GenBank
C. khinganensis **T**	HMJAU44507	China, Neimenggu	MT299952	OM001525	Xie et al. (2021b)
C. lewisii	iNAT130719864	USA	OP643406	–	GenBank
C. lilacinicarpus **T**	HMJAU58977	China, Fujian	PQ278675	PQ489270	Xie et al. (2025)
C. lilacinicarpus	KUN-HKAS81961	China, Guangdong	PQ278676	PQ489271	Xie et al. (2025)
C. microglobisporus **T**	IB20110123	Italy	NR_153027	–	Peintner et al. (2014)
C. mucifluus	TAAM128775	Estonia	UDB015965	–	Unite
C. mucobrunneus	HKAS 149456	China, Yunnan	PV992732	–	This study
C. mucobrunneus **T**	HKAS 149459	China, Yunnan	PV992733	PV992752	This study
C. obtusus	SAT00-298-30	USA	FJ717550	FJ717550	Harrower et al. (2011)
C. ochroglutinosus **T**	H7000818	Canada	NR_173073	–	Liimatainen and Niskanen 2021
C. parviviscidus	WTU-F-78349	Guyana	OR147297	PP468371	Siegel et al. (2024)
C. paveleckii **T**	Trappe 7962	USA	AF325564	–	Peintner et al. (2004)
C. paveleckii	OSC 62148	USA	KT968601	KU321878	GenBank
C. phlegmophorus **T**	Typus-M3	India	AY083186	–	Peintner et al. (2003)
C. porphyroideus	OTA:61406	New Zealand	JX178612	KT334150	Teasdale et al. (2013)
C. pseudocandelaris	UBC F17165 OC93	Canada	GQ159908	GQ159908	Harrower et al. (2011)
C. pseudosalor	MHHNU 32148	China, Hubei	OR660688	OR647505	Long et al. (2024)
C. pseudosalor **T**	MHHNU 32082	China, Hubei	OR660686	OR647504	Long et al. (2024)
C. putorius **T**	H T. Niskanen 07-411	USA	NR_153038	–	Ariyawansa et al. (2015)
C. pyrenaicus	JB-8573/15	Spain	KX239900	–	GenBank
C. rattinoides **T**	PDD:88283	New Zealand	JX000375	NG_064341	GenBank
C. rotundisporus	PERTH05255074	Australia	AY669612	AY669612	Garnica et al. (2005)
C. rotundisporus	G12	Australia	AF136738	–	Sawyer et al. (1999)
C. rugosiviscidus	HKAS 149457	China, Yunnan	PV992734	PV992753	This study
C. rugosiviscidus **T**	HKAS 149458	China, Yunnan	PV992735	PV992754	This study

Species	Voucher	Locality	GenBank Accession No.		References
			ITS	nrLSU	
C. salor	TUB011838	Germany	AY669592	AY669592	Garnica et al. (2005)
C. seidliae **T**	H:T. Niskanen 09-132	Finland	KR011125	KR011125	Ariyawansa et al. (2015)
C. septentrionalis	ARANFungi03516	Sweden	KX239915	–	GenBank
C. sinocalaisopus	HMJAU58978	China, Fujian	PQ278677	PQ489277	Xie et al. (2025)
C. sinocalaisopus **T**	HMJAU58984	China, Fujian	PQ278683	–	Xie et al. (2025)
C. sinosalor **T**	MHHNU30649	China, Hunan	PQ278661	PQ489281	Xie et al. (2025)
C. sinosalor	HMJAU58971	China, Zhejiang	PQ278662	PQ489282	Xie et al. (2025)
C. spilomeus **T**	S:CFP1137	Sweden	KX302267	–	Dima et al. (2016)
C. stillatitus	TUB 011587	Germany	AY669589	AY669589	Garnica et al. (2005)
C. subiodes **T**	K:M 001434108	USA	NR_190944	–	Liu et al. (2024)
C. subiodes	K:M 001434110	USA	ON843414	–	Liu et al. (2024)
C. subsalor	HMJAU48759	China, Zhejiang	MW911734	OP620670	Xie et al. (2021a)
C. subtropicus	MHHNU 31981	China, Hunan	OR660687	OR647502	Long et al. (2024)
C. subtropicus **T**	MHHNU 33533	China, Hunan	OR647488	OR647508	Long et al. (2024)
C. subviolaceus	AF69	Australia	DQ328114	–	GenBank
C. suecicolor **T**	PDD74698	New Zealand	JX000360	JX000391	GenBank
C. tabularis **T**	S:CFP949	Sweden	KX302275	–	Dima et al. (2016)
C. tasmacamphoratus	HO A20606A0	Tasmania	AY669633	AY669633	Garnica et al. (2005)
C. tessiae	PDD94054	New Zealand	JQ287698	–	GenBank
C. tessiae	PDD72611	New Zealand	HM060317	HM060316	GenBank
C. tianbaoyanensis	HMJAU58987	China, Fujian	PQ278685	PQ489283	Xie et al. (2025)
C. tibeticisalor	HMJAU48763	China, Xizang	MW911730	–	Xie et al. (2021a)
C. tibeticisalor **T**	HMJAU48764	China, Xizang	MW911729	OP620669	Xie et al. (2021a)
C. saloroides	HKAS 149460	China, Yunnan	PV992736	PV992755	This study
C. saloroides **T**	HKAS 149461	China, Yunnan	PV992737	PV992756	This study
C. vanduzerensis	VMS28	Canada	FJ717562	FJ717562	Harrower et al. (2011)
C. viridipileatus **T**	OTA64087	New Zealand	MK546593	MK546596	Nilsen et al. (2021)
C. vividus **T**	HMJAU58972	China, Chongqing	PQ278664	PQ489289	Xie et al. (2025)
C. vividus	HMJAU58974	China, Zhejiang	PQ278666	PQ489287	Xie et al. (2025)
Cortinarius sp.	SWUBC500	Canada	DQ481723	–	GenBank
Phlegmacium boreicyanites **T**	S:CFP931	Sweden	NR_130214	–	Liimatainen et al. (2014)
Ph. cyanites **T**	UPS A. Taylor 2005069	Sweden	NR_130233	–	Liimatainen et al. (2014)

Results

Molecular analyses

The concatenated matrix comprised 150 sequences (93 in ITS and 57 in nrLSU), representing 58 samples. Following Xie et al. (2021a), *Phlegmacium boreicyanites* (S: CFP931) and *P. cyanites* (UPS: A. Taylor 2005069) were treated as the outgroup taxa. The alignment contained 1,548 characters, including gaps (ITS: 1–647, nrLSU: 648–1,548), of which 1,061 characters were constant, 365 characters were parsimony-informative, and 122 were singleton sites. The estimated base frequencies were as follows: A = 0.258, C = 0.190, G = 0.244, T = 0.308, substitution rates AC = 1.81594, AG = 5.60442, AT = 1.81594, CG = 1.00000, CT = 8.94348, GT =

1.00000; and gamma distribution shape parameter α = 0.675. The ML and BI analyses showed similar topology, and the topology from the ML analysis was presented along with statistical values from the MLBS/BIPP algorithms (Fig. 1).

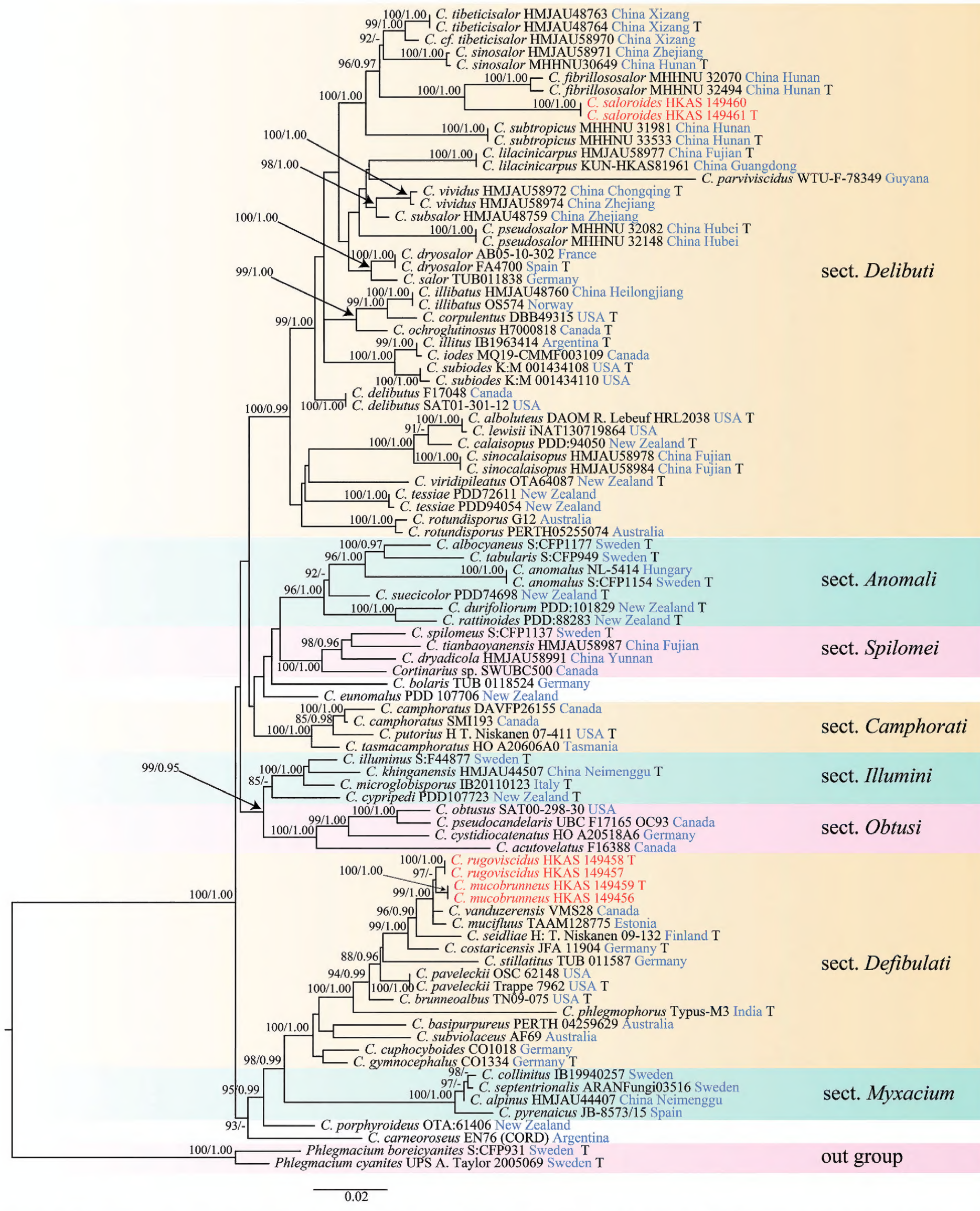
C. tibeticisalor HMJAU48763 China Xizang
C. tibeticisalor HMJAU48764 China Xizang T
C. cf. tibeticisalor HMJAU58970 China Xizang
C. sinosalor HMJAU58971 China Zhejiang
C. sinosalor MHHNU30649 China Hunan T
C. fibrillososalor MHHNU 32070 China Hunan
C. fibrillososalor MHHNU 32494 China Hunan T
C. saloroides HKAS 149460
C. saloroides HKAS 149461 T
C. subtropicus MHHNU 31981 China Hunan
C. subtropicus MHHNU 33533 China Hunan T
C. lilacinicarpus HMJAU58977 China Fujian T
C. lilacinicarpus KUN-HKAS81961 China Guangdong
C. parviviscidus WTU-F-78349 Guyana
C. vividus HMJAU58972 China Chongqing T
C. vividus HMJAU58974 China Zhejiang
C. subsalor HMJAU48759 China Zhejiang
C. pseudosalor MHHNU 32082 China Hubei T
C. pseudosalor MHHNU 32148 China Hubei
C. dryosalor AB05-10-302 France
C. dryosalor FA4700 Spain T
C. salor TUB011838 Germany
C. illibatus HMJAU48760 China Heilongjiang
C. illibatus OS574 Norway
C. corpulentus DBB49315 USA T
C. ochroglutinosus H7000818 Canada T
C. illitus IB1963414 Argentina T
C. iodes MQ19-CMMF003109 Canada
C. subiodes K:M 001434108 USA T
C. subiodes K:M 001434110 USA
C. delibutus F17048 Canada
C. delibutus SAT01-301-12 USA
C. alboluteus DAOM R. Lebeuf HRL2038 USA T
C. lewisii iNAT130719864 USA
C. calaisopus PDD:94050 New Zealand T
C. sinocalaisopus HMJAU58978 China Fujian
C. sinocalaisopus HMJAU58984 China Fujian T
C. viridipileatus OTA64087 New Zealand T
C. tessiae PDD72611 New Zealand
C. tessiae PDD94054 New Zealand
C. rotundisporus G12 Australia
C. rotundisporus PERTH05255074 Australia
C. albocyaneus S:CFP1177 Sweden T
C. tabularis S:CFP949 Sweden T
C. anomalus NL-5414 Hungary
C. anomalus S:CFP1154 Sweden T
C. suecicolor PDD74698 New Zealand T
C. durifoliorum PDD:101829 New Zealand T
C. rattinoides PDD:88283 New Zealand T
C. spilomeus S:CFP1137 Sweden T
C. tianbaoyanensis HMJAU58987 China Fujian
C. dryadicola HMJAU58991 China Yunnan
Cortinarius sp. SWUBC500 Canada
C. bolaris TUB 0118524 Germany
C. eunomalus PDD 107706 New Zealand
C. camphoratus DAVFP26155 Canada
C. camphoratus SMI193 Canada
C. putorius H T. Niskanen 07-411 USA T
C. tasmacamphoratus HO A20606A0 Tasmania
C. illuminus S:F44877 Sweden T
C. khinganensis HMJAU44507 China Neimenggu T
C. microglobisporus IB20110123 Italy T
C. cypripedi PDD107723 New Zealand T
C. obtusus SAT00-298-30 USA
C. pseudocandelaris UBC F17165 OC93 Canada
C. cystidiocatenatus HO A20518A6 Germany
C. acutovelatus F16388 Canada
C. rugoviscidus HKAS 149458 T
C. rugoviscidus HKAS 149457
C. mucobrunneus HKAS 149459 T
C. mucobrunneus HKAS 149456
C. vanduzerensis VMS28 Canada
C. mucifluus TAAM128775 Estonia
C. seidliae H: T. Niskanen 09-132 Finland T
C. costaricensis JFA 11904 Germany T
C. stillatitus TUB 011587 Germany
C. paveleckii OSC 62148 USA
C. paveleckii Trappe 7962 USA T
C. brunneoalbus TN09-075 USA T
C. phlegmophorus Typus-M3 India T
C. basipurpureus PERTH 04259629 Australia
C. subviolaceus AF69 Australia
C. cuphocyboides CO1018 Germany
C. gymnocephalus CO1334 Germany T
C. collinitus IB19940257 Sweden
C. septentrionalis ARANFungi03516 Sweden
C. alpinus HMJAU44407 China Neimenggu
C. pyrenaicus JB-8573/15 Spain
C. porphyroideus OTA:61406 New Zealand
C. carneoroseus EN76 (CORD) Argentina
Phlegmacium boreicyanites S:CFP931 Sweden T
Phlegmacium cyanites UPS A. Taylor 2005069 Sweden T
sect. Delibuti
sect. Anomali
sect. Spilomei
sect. Camphorati
sect. Illumini
sect. Obtusi
sect. Defibulati
sect. Myxacium
out group
0.02

Figure 1. Maximum likelihood phylogenetic tree generated from the combined ITS and nrLSU sequenced dataset. Maximum likelihood bootstrap (ML-BP) ≥ 85% and Bayesian posterior probabilities (BI-PP) ≥ 0.90 are indicated above the nodes. "-" indicates that the support value was less than the respective threshold. The specimen vouchers and country are indicated after the species names. New samples collected in this study are indicated in red. "T" indicates that the type specimens.

Phylogenetic analysis showed that all species formed separate monophyletic lineages. Our three new species are clustered in two different sections. *Cortinarius saloroides* clustered in sect. *Delibuti*, while *C. rugosiviscidus* and *C. mucobrunneus* clustered in sect. *Defibulati*. In sect. *Delibuti*, *Cortinarius saloroides*, and *C. fibrillososalor* were sister lineages (BP = 100%, PP = 1.00), forming a clade with *C. subtropicus* and *C. tibeticisalor*, which were only distributed in East Asia. In sect. *Defibulati*, *Cortinarius rugosiviscidus*, and *C. mucobrunneus* were sister lineages (BP = 97%), and had a close relationship with *C. vanduzerensis* and *C. mucifluus* (BP = 99%, PP = 1.00).

Taxonomy

Cortinarius mucobrunneus **T.S. Li, Y. Zhang & Q. Zhao, sp. nov**
MycoBank No: 860475
Fig. 2
Chinese name: 黏褐丝膜菌 (nian he si mo jun)

Etymology. mucobrunneus refers to the brown pileus with mucus on the surface.

Holotype. CHINA • Yunnan Province: Lijiang City, Laojunshan Nature Reserve, at 26.631426°N, 99.719085°E, alt. 3960 m, in *Abies* forest, 26 Aug. 2018, LJ1678 (HKAS 149459).

Diagnosis. Similar to *Cortinarius vanduzerensis* in the sticky pileus surface, but differing in the larger basidiospores.

Macrostructures. ***Basidiomata*** medium-sized. ***Pileus*** 40–60 mm diam., conical to campanulate, becoming applanate and umbonate with age; surface viscid, dark brown (7F8) to liver brown (8F8); margin tile red (7D8) to platinum blonde (4B3), undulate, translucent radially striate; context 4–5 mm thick at mid-radius, white. ***Lamellae*** adnate to adnexed, 3–4 mm broad, moderately crowded, cinnamon (6D4) to brown (6E7); edge serrate. ***Stipe*** 50–80 × 7–12 mm, cylindrical, usually tapering upwards; surface viscid, white, leaving a cinnamon (6D5) ring on the upper part of the stipe. Basal mycelium white. ***Odour*** not distinctive.

Microstructures. ***Basidiospores*** [100/2/2] (13–) 13.5–16 (–17) × 8–10 (–10.5) µm [Q = (1.42) 1.52–1.91 (–2), **Q** = 1.66 ± 0.09], elliptical to amygdaliform, cinnamon in KOH, strongly verrucose. ***Basidia*** 40–57 × 14–17 µm, clavate, 4-spored. ***Lamella trama*** hyphae 4–16 µm diam., smooth, colourless. Lamellar edges fertile. ***Pileipellis*** duplex: epicutis strongly gelatinous, 110–230 µm thick, composed of flat, loosely arranged, long-celled, colourless hyphae 4–10 µm diam.; hypocutis 35–70 µm thick, composed of cylindrical to elliptical, strongly interwoven, colourless hyphae 4–12 µm diam., some hyphae with spiral or spotted encrustations. ***Stipe hyphae*** 4–10 µm diam., colourless, smooth. ***Clamp connections*** absent.

Habitat. Mycorrhizal, gregarious in coniferous forests dominated by *Picea* spp. and *Abies* spp. trees.

Distribution. Known from the southern Yunnan Province, China.

Additional material examined. CHINA • Yunnan Province: Lijiang City, Laojunshan Nature Reserve, at 26.631426°N, 99.719085°E, alt. 3960 m, in *Abies* forest, 16 Aug. 2017, LJ981 (HKAS 149456).

Notes. *Cortinarius mucobrunneus* is characterized by its victid basidiomata, dark brown pileus with translucent stripes, cinnamon to brown lamellae, white stipe leaving a cinnamon ring on the upper part, and elliptical to amygdaliform, strongly warty basidiospores. Phylogenetic analysis indicates that *C. mucobrunneus* is nested in sect. *Defibulati* and is more closely related to *C. mucifluus* and *C. vanduzerensis* (Fig. 1). Morphologically, *C. mucobrunneus* showcases a dark brown pileus with tile red to platinum blonde margins alongside a white stipe, in contrast to *C. vanduzerensis* has a chestnut-black pileus with chestnut-brown margins and a light purple to dark lavender stipe (Smith and Trappe 1972). Furthermore, *C. mucobrunneus* has larger basidiospores [13–) 13.5–16 (–17) × 8–10 (–10.5) µm *vs.* (11–) 12–14 (–15) × 7–8 (–9) µm] than *C. vanduzerensis* (Smith and Trappe 1972). *Cortinarius mucobrunneus* is frequently misidentified as *C. mucifluus* due to the presence of translucent striations along the margin of the pileus, the pale stipe, and the

Figure 2. *Cortinarius mucobrunneus*. **a–c.** Basidiomata (**a, b.** HKAS 149459; **c.** HKAS 149456); **d.** Scanning electron micrograph of basidiospore; **e.** Basidiospores; **f, g.** Basidia; **h.** Pileipellis. Scale bars: 2 cm (**a–c**); 5 µm (**d**); 20 µm (**e–g**); 50 µm (**h**).

cinnamon-hued annulus situated on the upper portion of the stipe. Nevertheless, *C. mucobrunneus* is characterized by a dark brown to liver brown pileus that exhibits broader basidiospores, in contrast to the ochraceous brown pileus of *C. mucifluus*, which features comparatively narrower basidiospores.

Cortinarius rugosiviscidus **T.S. Li, Y. Zhang & Q. Zhao, sp. nov**

MycoBank No: 860476

Fig. 3

Chinese name: 皱粘丝膜菌 (zhou nian si mo jun)

Etymology. rugosiviscidus refers to the wrinkled and sticky surface of the pileus.

Holotype. CHINA • Yunnan Province: Lijiang City, Laojunshan Nature Reserve, at 26.631426°N, 99.719085°E, alt. 3960 m, in *Abies* forest, 25 Aug. 2018, LJ1634 (HKAS 149458).

Diagnosis. Similar to *Cortinarius mucobrunneus* in the sticky pileus surface, but differing in the lighter pileus color and shorter basidiospores.

Macrostructures. ***Basidioma*** medium-sized. ***Pileus*** 20–65 mm diam., hemispherical, conical to campanulate, becoming applanate and umbonate with age; surface viscid, wrinkled when mature, dark blonde (5D4) to dark brown (6F8), becoming light brown (6C3) when mature; margin no radially striated; context 3–6 mm thick at mid-radius, white, then turns reddish blonde (5C4). ***Lamellae*** adnate to adnexed, 4–8 mm broad, moderately crowded, first light reddish golden (6C5), later brown (6E6); edge serrate. ***Stipe*** 40–100 × 8–15 mm, cylindrical, slightly curved, usually tapering upwards, solid; surface viscid, the upper part light brown (6C3), the lower part white; context white, sometimes with dark blonde (5D4) bruises. Basal mycelium white. ***Odour*** not distinctive.

Microstructures. ***Basidiospores*** [150/2/2] (11–) 11.5–15 (–15.5) × (7–) 7.5–9.5 (–10) µm [Q = (1.32–) 1.35–1.73 (–1.85), **Q** = 1.55 ± 0.08], elliptical to amygdaliform, brown in KOH, moderately verrucose. ***Basidia*** 34–55 × 12–18 µm, clavate, 4-spored. Marginal elements (n = 20) 19–30 × 9–12 µm, broadly fusiform, elliptical. ***Lamella trama*** hyphae 4–12 µm diam., smooth, colourless. Lamellar edges fertile. ***Pileipellis*** duplex: epicutis strongly gelatinous, 300–385 µm thick, composed of cylindrical, loosely arranged, long-celled, colourless hyphae 4–7 µm diam.; hypocutis 90–150 µm thick, composed of cylindrical to elliptical, strongly interwoven, colourless hyphae 5–14 µm diam., some hyphae with spiral or spotted encrustations. ***Stipe hyphae*** 3–8 µm diam., colourless, smooth. ***Clamp connections*** absent.

Habitat. Mycorrhizal, gregarious in coniferous forests dominated by *Picea* and *Abies* trees.

Distribution. Known from the southern Yunnan Province, China.

Additional material examined. CHINA • Yunnan Province: Lijiang City, Laojunshan Nature Reserve, at 26.631426°N, 99.719085°E, alt. 3960 m, in *Abies* forest, 10 Aug. 2023, ZY13 (HKAS 149457).

Notes. *Cortinarius rugosiviscidus* is characterized by its victid basidiomata, light brown pileus with a wrinkled surface, brown lamellae, light brown stipe, and elliptical to amygdaliform basidiospores. Phylogenetic analysis indicates *C. rugosiviscidus*

Figure 3. *Cortinarius rugosiviscidus*. **a–c.** Basidiomata; (**a.** HKAS 149458; **b, c.** HKAS 149457); **d.** Scanning electron micrograph of basidiospore; **e.** Basidiospores; **f, g.** Basidia; **h.** Pileipellis. Scale bars: 2 cm (**a–c**); 5 μm (**d**); 20 μm (**e–g**); 50 μm (**h**).

is nested in sect. *Defibulati* sister branch to *C. mucobrunneus* (Fig. 1). Morphologically, *C. rugosiviscidus* showcases a light brown pileus with a light brown stipe, in contrast to *C. mucobrunneus*, which has a dark brown pileus and a white stipe.

Cortinarius saloroides **T.S. Li, Y. Zhang & Q. Zhao, sp. nov**

MycoBank No: 860477

Fig. 4

Chinese name: 类蓝紫丝膜菌 (lei lan zi si mo jun)

Etymology. saloroides refers to species that are morphologically similar to *Cortinarius salor*.

Holotype. CHINA • Yunnan Province: Pingbian County, Daweishan National Forest Park, at 22.963949°N 103.702776°E, alt. 2250 m, in the rainforest, 15 Jul. 2020, PB94 (HKAS 149461).

Diagnosis. Similar to *Cortinarius fibrillososalor* in the violaceous to whitish mauve pileus with fine fibrous scales, but differing in the thicker pileipellis.

Macrostructures. ***Basidioma*** small-sized. ***Pileus*** 15–45 mm diam., hemispherical to campanulate, becoming applanate and umbonate with age; surface dry, or viscid when wet, violet (17A8-17B8) to reddish violet (16B6), becoming mauve (17A5-17B5) when mature, with light brown (7D4) in the center and fine fibrous scales; margin inrolled when young, with remnants of universal veil; context 2–3 mm thick at mid-radius, white. ***Lamellae*** adnate to adnexed, 2–4 mm broad, moderately crowded, first white to mauve (17A5-17B5), later light brown (7D4); edge crenate. ***Stipe*** 20–50 × 4–6 mm, cylindrical, curved, usually tapering upwards; surface dry, bluish violet (18B6) or slightly lighter, leaving a light brown (7D4) ring on the upper part of the stipe; context white. Basal mycelium white. ***Odour*** not distinctive.

Microstructures. ***Basidiospores*** [100/2/2] 7–8.5 (–9) × (5–) 5.5–6.5 (–7) µm [Q = 1.11–1.38, **Q** = 1.24 ± 0.06], subspherical, broadly elliptical to elliptical, light brown to dark brown in KOH, moderately verrucose. ***Basidia*** 24–36 × 7–10 µm, clavate, 4-spored. ***Lamella trama*** hyphae 6–22 µm diam., smooth, colourless. Lamellar edges fertile. ***Pileipellis*** duplex: epicutis strongly gelatinous, 225–370 µm thick, composed of cylindrical, loosely arranged, long-celled, colourless hyphae 4–14 µm diam.; hypocutis 90–120 µm thick, composed of cylindrical to elliptical, strongly interwoven, colourless hyphae 8–23 µm diam., some hyphae with spiral or spotted encrustations. ***Stipe hyphae*** 3–10 µm diam., colourless, smooth. ***Clamp connections*** present. Cystidia absent.

Habitat. Mycorrhizal, gregarious on the ground in tropical rainforests.

Figure 4. *Cortinarius saloroides*. **a, b.** Basidiomata (**a.** HKAS 149460; **b.** HKAS 149461); **c.** Pileipellis; **d.** Scanning electron micrograph of basidiospore; **e.** Basidiospores; **f, g.** Basidia. Scale bars: 2 cm (**a, b**); 50 µm (**c**); 2 µm (**d**); 10 µm (**e–g**).

Distribution. Known from the southern Yunnan Province, China.

Additional material examined. CHINA • Yunnan Province: Pingbian County, Daweishan National Forest Park, at 22.963949°N 103.702776°E, alt. 2250 m, in the rainforest, 29 Jul. 2019, PB-DWS 391 (HKAS 149460).

Notes. *Cortinarius saloroides* is characterized by its violet pileus with fine fibrous scales, mauve to light brown lamellae, bluish violet stipe leaving a light brown ring on the upper part, and subspherical, broadly elliptical to elliptical basidiospores. Phylogenetic analysis indicates that *C. saloroides* is nested in sect. *Delibuti* sister branch to *C. fibrillososalor* (Fig. 1). Morphologically, *C. saloroides* showcases a violet pileus with fine fibrous scales on the surface and a bluish violet stipe, which can be confused with *C. fibrillososalor*. Nevertheless, *C. saloroides* can be distinguished from *C. fibrillososalor* by its thicker pileipellis, wider stipe hyphae, and slightly smaller basidiospores (Long et al. 2024).

Discussion

Based on morphological characteristics and phylogenetic analysis of the ITS+LSU dataset, this study describes three new species of the genus *Cortinarius*, namely *C. mucobrunneus*, *C. rugosiviscidus*, and *C. saloroides*. In the phylogenetic framework, *C. saloroides* was positioned within sect. *Delibuti*, whereas *C. mucobrunneus* and *C. rugosiviscidus* were classified within sect. *Defibulati*.

Section *Delibuti* represents a highly diverse lineage, encompassing 16 newly described species in recent years (Ammirati 2018; Liimatainen and Niskanen 2021; Xie et al. 2021a; Bhunjun et al. 2022; Crous et al. 2022; Bojantchev 2023; Liu et al. 2024; Long et al. 2024; Siegel et al. 2024; Xie et al. 2025). The morphological characteristics of species within section *Delibuti* encompass a range of fruiting body colors, including blue, yellow, brown, or green; the pileus exhibits a sticky to viscous texture, while the lamellae exhibit a pale blue-purple hue that transitions to brown upon maturation. Additionally, mucus may be present, often accompanied by an annular zone located on the upper portion of the stipe. Basidiospores are observed to be nearly spherical to broadly elliptical in shape. (Peintner et al. 2004; Garnica et al. 2005; Soop et al. 2019). The newly described *Cortinarius saloroides* aligns morphologically with the characteristics of section *Delibuti* and is phylogenetically nested within this section. It forms a lineage with *C. fibrillososalor*, *C. sinosalor*, *C. subtropicus*, and *C. tibeticisalor*, which are characterized by violet pileus and are restricted to East Asia, consistent with Long et al. (2024). *Cortinarius fibrillososalor* can be well distinguished from other species in the sect. *Delibuti* by the fibrils on the surface of the pileus (Long et al. 2024). It is worth noting that *C. saloroides* exhibits a similar trait, making it challenging to differentiate from *C. fibrillososalor* by macroscopic morphology. Currently, within the sect. *Delibuti*, two species are identified that possess a violet pileus and fibrillose surface texture. Nonetheless, these species can be distinguished by the thickness of the pileipellis, the width of the stipe hyphae, and the length of the basidiospores. Furthermore, BLAST analysis has indicated that the ITS sequence of *Cortinarius saloroides* shows 92.51% similarity to that of the type specimen of *C. fibrillososalor*, with 53 nucleotide substitutions and insertion-deletion (indel) positions.

In sect. *Defibulati*, species exhibit consistent morphological characteristics, mainly including: the pileus and stipe covered with mucus, relatively large elliptical to amygdaliform basidiospores with warty surfaces, the absence of clamp connections, and incomplete development of the veil, among other features (Ammirati et al. 2007; Soop et al. 2021). Additionally, ITS sequences of species in this section show minimal variation, differing by only 2–3 base sites (Seidl 2000). The other two new species described in this study, *Cortinarius mucobrunneus* and *C. rugosiviscidus*, are nested in sect. *Defibulati* based on phylogenetic analysis. They form sister clades and are closely related to *C. mucifluus* and *C. vanduzerensis*. Morphologically, the stipe of *C. vanduzerensis* is light purple to dark lavender, differing from the white stipe of *C. mucobrunneus* and the brownish stipe of *C. rugosiviscidus*. The pileus of *Cortinarius rugosiviscidus* is dark blonde to dark brown, contrasting with the ochraceous brown pileus of *C. mucifluus*. BLAST analysis showed that the ITS sequence of *C. mucobrunneus* is most similar to that of *C. vanduzerensis* (FJ717562), with 98.65% similarity and 12 substitutions/indels. Similarly, the ITS sequence of *C. rugosiviscidus* is closely related to *C. vanduzerensis* (FJ717562), showing 98.38% similarity and 13 substitutions/indels. A total of 8 substitutions/indels were observed between the ITS sequences of the type specimens of *C. mucobrunneus* and *C. rugosiviscidus*. Both morphological and molecular evidence confirm that *C. mucobrunneus* and *C. rugosiviscidus* are distinct, independent species within sect. *Defibulati*.

Cortinarius has established itself as a paramount taxonomic clade in mycology, distinguished by its remarkable species diversity, essential ecological roles, and complex classification structure. Advances in molecular systematics have significantly enhanced our understanding of the genus's classification, phylogenetic relationships, and associated ecological functions (Wang et al. 2025). Historically, species identification was predominantly based on morphological traits prior to the incorporation of molecular data. In China, where research in fungal taxonomy has lagged behind that of other regions, numerous species within the genus *Cortinarius* have been inaccurately classified alongside their European or American counterparts (Xie et al. 2023). As it is renowned for possessing one of the most diverse fungal ecosystems worldwide, particularly within biodiversity hotspots like Yunnan, China, it harbours a significant array of endemic and unique *Cortinarius* species. However, historical constraints in research methodologies have hindered a thorough elucidation of the taxonomic status and true diversity of these taxa.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Methodology, Tai-Shun Li; Formal analysis, Tai-Shun Li and Ying Zhang; Investigation, Qi Zhao and Ying Zhang; Resources, Qi Zhao and Ying Zhang; Data curation, Tai-Shun Li, Hong-Bin Guan, Yan-Yan Yang; Writing–Original draft preparation, Tai-Shun Li; Writing–Review and editing, Fang Wu, Qi Zhao and Ying Zhang; Funding acquisition, Qi Zhao and Ying Zhang.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

Ammirati J (2018) Nomenclatural novelties. Index Fungorum : Published Numbers 363: 1. https://www.indexfungorum.org/Publications/Index%20Fungorum%20no.363.pdf

Ammirati J, Garnica S, Halling RE, Mata M, Mueller GM, Carranza J (2007) New *Cortinarius* species associated with *Quercus* and *Comarostaphylis* in Costa Rica. Botany 85(9): 794–812. https://doi.org/10.1139/B07-067

Ariyawansa HA, Hyde KD, Jayasiri SC, Buyck B, Chethana KWT, Dai DQ, Dai YC, Daranagama DA, Jayawardena RS, Lücking R, Ghobad-Nejhad M, Niskanen T, Thambugala KM, Voigt K, Zhao RL, Li GJ, Doilom M, Boonmee S, Yang ZL, Cai Q, Cui YY, Bahkali AH, Chen J, Cui BK, Chen JJ, Dayarathne MC, Dissanayake AJ, Ekanayaka AH, Hashimoto A, Hongsanan S, Jones EBJ, Larsson E, Li WJ, Li QR, Liu JK, Luo ZL, Maharachchikumbura SSN, Mapook A, McKenzie EHC, Norphanphoun C, Konta S, Pang KL, Perera RH, Phookamsak R, Phukhamsakda C, Pinruan U, Randrianjohany E, Singtripop C, Tanaka K, Tian CM, Tibpromma S, Abdel-Wahab MA, Wanasinghe DN, Wijayawardene NN, Zhang JF, Zhang H, Abdel-Aziz FA, Wedin M, Westberg M, Ammirati JF, Bulgakov TS, Lima DX, Callaghan TM, Callac P, Chang CH, Coca LF, Dal-Forno M, Dollhofer V, Fliegerová K, Greiner K, Griffith GW, Ho HM, Hofstetter V, Jeewon R, Kang JC, Wen TC, Kirk PM, Kytövuori I, Lawrey

JD, Xing J, Li H, Liu ZY, Liu XZ, Liimatainen K, Lumbsch HT, Matsumura M, Moncada B, Nuankaew S, Parnmen S, Santiago ALCMA, Sommai S, Song Y, Souza CAF, Souza-Motta CM, Su HY, Suetrong S, Wang Y, Wei SF, Wen TC, Yuan HS, Zhou LW, Réblová M, Fournier J, Camporesi E, Luangsa-ard JJ, Tasanathai K, Khonsanit A, Thanakitpipattana D, Somrithipol S, Diederich P, Millanes AM, Common RS, Stadler M, Yan JY, Li XH, Lee HW, Nguyen TTT, Lee HB, Battistin E, Marsico O, Vizzini A, Vila J, Ercole E, Eberhardt U, Simonini G, Wen HA, Chen XH, Miettinen O, Spirin V (2015) Fungal diversity notes 111–252-taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 75(1): 27. https://doi.org/10.1007/s13225-015-0346-5

Bau T, Li HJ, Bao HY, Li Y (2024) A Revised Checklist of Poisonous Mushrooms in China. Journal of Fungal Research 22(4): 301–321. https://doi.org/10.13341/j.jfr.2024.0010

Bendiksen E, Bendiksen K, Brandrud TE (1993) *Cortinarius* subgenus *Myxacium* section *Colliniti* (Agaricales) in Fennoscandia, with special emphasis on the Arctic-alpine zones. Sommerfeltia 19: 1–37. https://doi.org/10.2478/som-1993-0005

Bhunjun CS, Niskanen T, Suwannarach N, Wannathes N, Chen YJ, McKenzie EHC, Maharachchikumbura SSN, Buyck B, Zhao CL, Fan YG, Zhang JY, Dissanayake AJ, Marasinghe DS, Jayawardena RS, Kumla J, Padamsee M, Chen YY, Liimatainen K, Ammirati JF, Phukhamsakda C, Liu JK, Phonrob W, Randrianjohany É, Hongsanan S, Cheewangkoon R, Bundhun D, Khuna S, Yu WJ, Deng LS, Lu YZ, Hyde KD, Lumyong S (2022) The numbers of fungi: Are the most speciose genera truly diverse? Fungal Diversity 114: 387–462. https://doi.org/10.1007/s13225-022-00501-4

Bojantchev D (2023) Nomenclatural novelties. Index Fungorum: Published Numbers 565: 1–12. https://www.indexfungorum.org/Publications/Index%20Fungorum%20no.565.pdf

Brandrud TE, Lindstrom H, Marklund H, Melot J, Muskos S (1990) *Cortinarius* Flora Photographica I (English version). *Cortinarius* HB, Matfors, 60 pp.

Brandrud TE, Lindstrom H, Marklund H, Melot J, Muskos S (1992) *Cortinarius* Flora Photographica II (English version). *Cortinarius* HB, Matfors, 60 pp.

Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T (2009) trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics (Oxford, England) 25: 1972–1973. https://doi.org/10.1093/bioinformatics/btp348

Crous PW, Boers J, Holdom D, Steinrucken TV, Tan YP, Vitelli JS, Shivas RG, Barrett M, Boxshall AG, Broadbridge J, Larsson E (2022) Fungal Planet description sheets: 1383–1435. Persoonia-Molecular Phylogeny and Evolution of Fungi 48(1): 261–371. https://doi.org/10.3767/persoonia.2022.48.08

Dima B, Lindström H, Liimatainen K, Olson Å, Soop K, Kytövuori I, Dahlberg A, Niskanen T (2016) Typification of Friesian names in *Cortinarius* sections *Anomali*, *Spilomei*, and *Bolares*, and description of two new species from northern Europe. Mycological Progress 15(9): 903–919. https://doi.org/10.1007/s11557-016-1217-5

Dima B, Liimatainen K, Niskanen T, Bojantchev D, Harrower E, Papp V, Nagy LG, Kovács GM, Ammirati JF (2021) Type studies and fourteen new North American species of *Cortinarius* section *Anomali* reveal high continental species diversity. Mycological Progress 20(11): 1399–1439. https://doi.org/10.1007/s11557-021-01738-0

Earle FS (1902) A key to the North American species of *Cortinarius*.—I. Torreya 2(11): 169–172.

Garnica S, Weiß M, Oertel B, Oberwinkler F (2005) A framework for a phylogenetic classification in the genus *Cortinarius* (Basidiomycota, Agaricales) derived from morphological and molecular data. Botany 83(11): 1457–1477. https://doi.org/10.1139/b05-107

Gray SF (1821) A Natural Arrangement of British plants. Baldwin, Cradock and Joy, London, 627–630.

Harrington TJ, Mitchell DT (2002) Colonization of root systems of *Carex flacca* and *C. pilulifera* by *Cortinarius* (*Dermocybe*) *cinnamomeus*. Mycological Research 106(4): 452–459. https://doi.org/10.1017/S0953756202005713

Harrower E, Ammirati JF, Cappuccino AA, Ceska O, Kranabetter JM, Kroeger P, Lim SR, Taylor T, Berbee ML (2011) *Cortinarius* species diversity in British Columbia and molecular phylogenetic comparison with European specimen sequences. Botany 89(11): 799–810. https://doi.org/10.3852/14-182

Harrower E, Bougher NL, Henkel TW, Horak E, Matheny PB (2015) Long-distance dispersal and speciation of Australasian and American species of *Cortinarius* sect. *Cortinarius*. Mycologia 107(4): 697–709. https://doi.org/10.3852/14-182

Hu Y, Karunarathna SC, Li H, Galappaththi MC, Zhao CL, Kakumyan P, Mortimer PE (2022) The impact of drying temperature on basidiospore size. Diversity 14(4): 239. https://doi.org/10.3390/d14040239

Jacquemyn H, Honnay O, Cammue BP, Brys R, Lievens B (2010) Low specificity and nested subset structure characterize mycorrhizal associations in five closely related species of the genus *Orchis*. Molecular Ecology 19(18): 4086–4095. https://doi.org/10.1111/j.1365-294X.2010.04785.x

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30: 772–780. https://doi.org/10.1093/molbev/mst010

Katoh K, Rozewicki J, Yamada KD (2019) MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20: 1160–1166. https://doi.org/10.1093/bib/bbx108

Kornerup A, Wanscher JH (1981) Taschenlexikon der Farben: 1440 Farbnuancen und 600 Farbnamen. 3rd ed. Muster-Schmidt Verlag, Göttingen.

Liimatainen K, Niskanen T (2021) Nomenclatural novelties. Index Fungorum: Published Numbers 487: 1–7. https://www.indexfungorum.org/Publications/Index%20Fungorum%20no.487.pdf

Liimatainen K, Niskanen T, Dima B, Kytövuori I, Ammirati JF, Frøslev TG (2014) The largest type study of Agaricales species to date: Bringing identification and nomenclature of *Phlegmacium* (*Cortinarius*) into the DNA era. Persoonia 33(1): 98–140. https://doi.org/10.3767/003158514X684681

Liu SL, Wang XW, Li GJ, Deng CY, Rossi W, Leonardi M, Liimatainen K, Kekki T, Niskanen T, Smith ME, Ammirati J, Bojantchev D, Abdel-Wahab MA, Zhang M, Tian Ej, Lu YZ, Zhang JY, Ma J, Dutta AK, Acharya K, Du TY, Xu J, Kim JS, Lim YW, Gerlach A, Zeng NK, Han YX, Razaghi P, Raza M, Cai L, Calabon MS, Jones EBG, Saha R, Kumar TKA, Krishnapriya K, Thomas A, Kaliyaperumal M, Kezo K, Gunaseelan S, Singh SK, Singh PN, Lagashetti AC, Pawar KS, Jiang SH, Zhang C, Zhang H, Qing Y, Bau T, Peng XC, Wen TC, Ramirez NA, Niveiro N, Li MX, Yang ZL, Wu G, Tarafder E, Tennakoon DS, Kuo CH, Silva TM, Souza-Motta CM, Bezerra JDP, He G, Ji XH, Suwannarach N, Kumla J, Lumyong S, Wannathes N, Rana S, Hyde KD, Zhou LW (2024) Fungal diversity notes 1717–1817: Taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity 124(1): 1–216. https://doi.org/10.1007/s13225-023-00529-0

Long P, Zhou SY, Li SN, Liu FF, Chen ZH (2024) Three new species of *Cortinarius* section *Delibuti* (Cortinariaceae, Agaricales) from China. MycoKeys 101: 143. https://doi.org/10.3897/mycokeys.101.114705

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. 2010 Gateway Computing Environments Workshop (GCE), 1–8. https://doi.org/10.1109/GCE.2010.5676129

Moser MM, Horak E (1975) *Cortinarius* Fr. und nahe verwandte Gattungen in Südamerika. Nova Hedwigia. Beiheft 52: 1–628.

Nilsen AR, Macrae OC, Andrew KM, Wang XY, Tana MCT, Soop K, Brown CM, Summerfield TC, Orlovich DA (2021) Studies of New Zealand *Cortinarius*: Resolution of taxonomic conflicts in section *Subcastanelli* (Agaricales), new species and key to rozitoid species. New Zealand Journal of Botany 59(4): 457–475. https://doi.org/10.1080/0028825X.2021.1879877

Niskanen T, Kytövuori I, Liimatainen K, Ammirati JF (2015) Nomenclatural novelties. Index Fungorum: Published Numbers 256: 1–2.

Nylander JA, Ronquist F, Huelsenbeck JP, Nieves-Aldrey J (2004) Bayesian phylogenetic analysis of combined data. Systematic Biology 53: 47–67. https://doi.org/10.1080/10635150490264699

Peintner U, Horak E, Moser MM, Vilgalys R (2002) Phylogeny of *Rozites*, *Cuphocybe* and *Rapacea* inferred from ITS and LSU rDNA sequences. Mycologia 94(4): 620–629. https://doi.org/10.1080/15572536.2003.11833190

Peintner U, Moser MM, Thomas KA, Manimohan P (2003) First records of ectomycorrhizal *Cortinarius* species (Agaricales, Basidiomycetes) from tropical India and their phylogenetic position based on rDNA ITS sequences. Mycological Research 107(4): 485–494. https://doi.org/10.1017/S0953756203007585

Peintner U, Moncalvo JM, Vilgalys R (2004) Toward a better understanding of the in frageneric relationships in *Cortinarius* (Agaricales, Basidiomycota). Mycologia 96(5): 1042–1058. https://doi.org/10.1080/15572536.2005.11832904

Peintner U, Dresch P, Bellú F, Borghi E (2014) *Cortinarius microglobisporus* (Basidiomycota), a new species with roundish spores related to *C. illuminus*. Mycological Progress 13(3): 899–904. https://doi.org/10.1007/s11557-014-0975-1

Persoon DCH (1801) Synopsis Methodica Fungorum. Aivd Henricum Dieterich, Göttingen, 276–301.

Rathnayaka AR, Tennakoon DS, Jones GE, Wanasinghe DN, Bhat DJ, Priyashantha AH, Stephenson SL, Tibpromma S, Karunarathna SC (2024) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. New Zealand Journal of Botany 63(2–3): 462–489. https://doi.org/10.1080/0028825X.2024.2381734

Sawyer NA, Chambers SM, Cairney JWG (1999) Molecular investigation of genet distribution and genetic variation of *Cortinarius rotundisporus* in eastern Australian sclerophyll forests. The New Phytologist 142(3): 561–568. https://doi.org/10.1046/j.1469-8137.1999.00417.x

Seidl MT (2000) Phylogenetic relationships within *Cortinarius* subgenus *Myxacium*, sections *Defibulati* and *Myxacium*. Mycologia 92(6): 1091–1102. https://doi.org/10.1080/00275514.2000.12061257

Siegel N, Henkel TW, Adams S, Cooper J, Aime MC (2024) New Cortinariaceae species associated with Dicymbe, Aldina, and Pakaraimaea in Guyana. Mycologia 116(5): 848–864. https://doi.org/10.1080/00275514.2024.2367399

Singer R (1986) The Agaricales in modern taxonomy. 4th Ed. Koeltz Scientific Books, Keonigstein, 1–981.

Smith AH, Trappe JM (1972) The Higher Fungi of Oregon's Cascade Head Experimental Forest and Vicinity—I. The Genus *Phaeocollybia* (Agaricales) and Notes and Descriptions of Other Species in the Agaricales. Mycologia 64(5): 1138–1153. https://doi.org/10.1080/00275514.1972.12019358

Soop K (2016) A contribution to the study of the cortinarioid mycoflora of New Zealand, VII. New Zealand Journal of Botany 54(3): 344–365. https://doi.org/10.1080/0028825X.2016.1178149

Soop K, Wallace M, Dima B (2018) New *Cortinarius* (Agaricales) species described from New Zealand. New Zealand Journal of Botany 56(2): 163–182. https://doi.org/10.1080/0028825X.2018.1436574

Soop K, Dima B, Cooper JA, Park D, Oertel B (2019) A phylogenetic approach to a global supraspecific taxonomy of *Cortinarius* (Agaricales) with an emphasis on the southern mycota. Persoonia-Molecular Phylogeny and Evolution of Fungi 42(1): 261–290. https://doi.org/10.3767/persoonia.2019.42.10

Soop K, Nilsen AR, Orlovich DA, Dima B (2021) An emended subgenus *Myxacium* in the light of a global *Cortinarius* (Agaricales) phylogeny. Mycological Progress 20(3): 247–260. https://doi.org/10.1007/s11557-020-01665-6

Stensrud Ø, Orr RJ, Reier-Røberg K, Schumacher T, Høiland K (2014) Phylogenetic relationships in *Cortinarius* with focus on North European species. Karstenia 54(2): 57–71. https://doi.org/10.29203/ka.2014.464

Teasdale SE, Beulke AK, Guy PL, Orlovich DA (2013) Environmental barcoding of the ectomycorrhizal fungal genus *Cortinarius*. Fungal Diversity 58(1): 299–310. https://doi.org/10.1007/s13225-012-0218-1

Tedersoo L, Bahram M, Jairus T, Bechem E, Chinoya S, Mpumba R, Leal M, Randrianjohany E, Razafimandimbison S, Sadam AVE, Naadel T (2011) Spatial structure and the effects of host and soil environments on communities of ectomycorrhizal fungi in wooded savannas and rain forests of Continental Africa and Madagascar. Molecular Ecology 20(14): 3071–3080. https://doi.org/10.1111/j.1365-294X.2011.05145.x

Thoen E, Aas AB, Vik U, Brysting AK, Skrede I, Carlsen T, Kauserud H (2019) A single ectomycorrhizal plant root system includes a diverse and spatially structured fungal community. Mycorrhiza 29(3): 167–180. https://doi.org/10.1007/s00572-019-00889-z

Trog JG (1844) Verzeichniss schweizerischer Schwämme, welche grösstentheils in der Umgebung von Thun gesammelt worden sind. Mitteilungen der Naturforschenden Gesellschaft Bern 1844(15–23): 17–92.

Vaidya G, Lohman DJ, Meier R (2011) SequenceMatrix: Concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics: The International Journal of the Willi Hennig Society 27: 171–180. https://doi.org/10.1111/j.1096-0031.2010.00329.x

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Wang XH, Cai Q, Yu FM, Yang ZL, Zhou SY, Wang ZR, Cui YY, Wang Y, Zhang P, Cao SQ, Zhu XT, Lei L, Lu JR, Li JN, Wang GS, Jia LK, Mu LH, Li GM, Li MX, Yang BQ, Feng WC, Liu ZW, Li CJY, Xu RJ, Bao SX, Li TS, Jia PS, Wu DM, Gao N, Hyde KD, Wu G, Zhao Q (2025) New and notable Basidiomycota on the Qinghai-Xizang

Plateau and its surrounding areas. Fungal Diversity 133, 235–437. https://doi.org/10.1007/s13225-025-00558-x

White TJ, Bruns T, Lee SJWT, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR protocols: a guide to methods and applications 18: 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Xie ML, Chen JL, Phukhamsakda C, Dima B, Fu YP, Ji RQ, Wang K, Wei TZ, Li Y (2021a) *Cortinarius subsalor* and *C. tibeticisalor* spp. nov., two new species from the section *Delibuti* from China. PeerJ 9: e11982. https://doi.org/10.7717/peerj.11982

Xie ML, Wei TZ, Dima B, Fu YP, Ji RQ, Li Y (2021b) *Cortinarius khinganensis* (Agaricales), a new species of section Illumini from northeast China. Phytotaxa 500(1): 1–10. https://doi.org/10.11646/phytotaxa.500.1.1

Xie ML, Wei TZ, Ji RQ, Li Y, Li Y (2023) Research progress on taxonomy system and species diversity of *Cortinarius*. Journal of Fungal Research 21(Z1): 103–112. https://doi.org/10.13341/j.jfr.2023.1594

Xie ML, Yu Y, Long P, Chen ZH, Wang ZR, Ma HX, Wei TZ, Liao JP, Li CT, Yang ZQ, Li Y (2025) New insights into *Cortinarius*: Novel taxa from subtropical China. Mycology: 1–19. https://doi.org/10.1080/21501203.2024.2434584

Zhao Q, Bau T, Zhao YC, Yang ZL, Hyde KD (2015) Species diversity within the *Helvella crispa* group (Ascomycota: Helvellaceae) in China. Phytotaxa 239(2): 130–142. https://doi.org/10.11646/phytotaxa.239.2.2